SEQUENCE LISTING

<110> Bristol-Myers Squibb Company

<120> POLYNUCLEOTIDE ENCODING TWO NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBUNITS, K+betaM4 and K+betaM5

<130> D0115NP

<150> US 60/272,190
<151> 2001-02-28

<150> US 60/274,258
<151> 2001-03-07

<160> 98

<170> PatentIn version 3.0

<210> 1
<211> 1839
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (5)..(1057)

<400> 1

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acaa atg acc ggg agc cat gac gtc atc ggg ggc gca gga aag cag gtg        49
     Met Thr Gly Ser His Asp Val Ile Gly Gly Ala Gly Lys Gln Val
     1               5                   10                  15

ctc tgc tgc ttt tgc aag cag aga aat aag agt ttg ggc acc tac cca        97
Leu Cys Cys Phe Cys Lys Gln Arg Asn Lys Ser Leu Gly Thr Tyr Pro
                20                  25                  30

ggg gtc cca ggg aat gcc ctg tgg ctc ctg acc tcc ccc gcc tgt aat       145
Gly Val Pro Gly Asn Ala Leu Trp Leu Leu Thr Ser Pro Ala Cys Asn
            35                  40                  45

gct ctg agc act tca gca gta atg cat gga aga gat aag ggg tct gtg       193
Ala Leu Ser Thr Ser Ala Val Met His Gly Arg Asp Lys Gly Ser Val
            50                  55                  60

acc cat gga act gtc caa gtc ctc tct gac acc cgc ttc ttt tcc tgc       241
Thr His Gly Thr Val Gln Val Leu Ser Asp Thr Arg Phe Phe Ser Cys
    65                  70                  75

cgt gaa gga cta ctt cca gca acc cag tct cct gcc atg tcc gac ccc       289
Arg Glu Gly Leu Leu Pro Ala Thr Gln Ser Pro Ala Met Ser Asp Pro
80                  85                  90                  95

atc acg ctg aac gtc ggg ggg aag ctc tat aca acc tca ctg gcg acc       337
Ile Thr Leu Asn Val Gly Gly Lys Leu Tyr Thr Thr Ser Leu Ala Thr
                100                 105                 110
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1

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ctg acc agc ttc cct gac tcc atg cta ggc gcc atg ttc agc ggg aag          385
Leu Thr Ser Phe Pro Asp Ser Met Leu Gly Ala Met Phe Ser Gly Lys
            115             120             125

atg ccc acc aag agg gac agc cag ggc aac tgc ttc att gac cgt gac          433
Met Pro Thr Lys Arg Asp Ser Gln Gly Asn Cys Phe Ile Asp Arg Asp
            130             135             140

ggc aaa gtg ttc cgc tat atc ctc aac ttc ctg cgg acc tcc cac ctt          481
Gly Lys Val Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser His Leu
            145             150             155

gac ctg cct gag gac ttc cag gag atg ggg ctg ctc cgc agg gag gcc          529
Asp Leu Pro Glu Asp Phe Gln Glu Met Gly Leu Leu Arg Arg Glu Ala
160             165             170             175

gac ttc tac cag gtg cag ccc ctg att gag gcc ctg cag gag aag gaa          577
Asp Phe Tyr Gln Val Gln Pro Leu Ile Glu Ala Leu Gln Glu Lys Glu
                180             185             190

gtg gag ctc tcc aag gcc gag aag aat gcc atg ctc aac atc aca ctg          625
Val Glu Leu Ser Lys Ala Glu Lys Asn Ala Met Leu Asn Ile Thr Leu
                195             200             205

aac cag cgt gtg cag acg gtc cac ttc act gtg cgc gag gca ccc cag          673
Asn Gln Arg Val Gln Thr Val His Phe Thr Val Arg Glu Ala Pro Gln
            210             215             220

atc tac agc ctc tcc tct tcc agc atg gag gtc ttc aac gcc aac atc          721
Ile Tyr Ser Leu Ser Ser Ser Ser Met Glu Val Phe Asn Ala Asn Ile
            225             230             235

ttc agc acc tcc tgc ctc ttc ctc aag ctc ctt ggc tct aag ctc ttc          769
Phe Ser Thr Ser Cys Leu Phe Leu Lys Leu Leu Gly Ser Lys Leu Phe
240             245             250             255

tac tgc tcc aat ggc aat ctc tcc tcc atc acc agc cac ttg cag gac          817
Tyr Cys Ser Asn Gly Asn Leu Ser Ser Ile Thr Ser His Leu Gln Asp
                260             265             270

ccc aac cac ctg act ctg gac tgg gtg gcc aat gtg gag ggc ctg cca          865
Pro Asn His Leu Thr Leu Asp Trp Val Ala Asn Val Glu Gly Leu Pro
            275             280             285

gag gag gag tac acc aag cag aac ctc aag agg ctc tgg gtg gtg ccc          913
Glu Glu Glu Tyr Thr Lys Gln Asn Leu Lys Arg Leu Trp Val Val Pro
            290             295             300

gcc aac aag cag atc aac agc ttc cag gtc ttc gtg gaa gag gta ctg          961
Ala Asn Lys Gln Ile Asn Ser Phe Gln Val Phe Val Glu Glu Val Leu
            305             310             315

aaa atc gct ctg agc gat ggc ttc tgc atc gat tct tct cac cca cat          1009
Lys Ile Ala Leu Ser Asp Gly Phe Cys Ile Asp Ser Ser His Pro His
320             325             330             335

gct ctg gat ttt atg aac aat aag att att cga tta ata cgg tac agg          1057
```

2

```
Ala Leu Asp Phe Met Asn Asn Lys Ile Ile Arg Leu Ile Arg Tyr Arg
            340                 345                 350

taaaaggacc ccaacaacac tggagatggg gagtcccagg aagctcatgt cagccaggtc   1117

ttggagggca tctcgccagt ggtgcgaggc aggggactat actaatctgt attaattgtg   1177

tagcaggact tgattccccc catgatgaag tccacctttt ggaatccagt gtcctctgaa   1237

cagaaccacc ttttttcttg ccattttgag ctgcagacag cggtttatt atgacaagtg    1297

aagagtcagc tgatgtgtac taaaggaggc ataggagga ttttccagcc aggacaaaag    1357

agcagcagtt ttctcctggg ctccatctct ctgtaccgct agccagtgcc gcatttatcc   1417

atctgtaaga aggccctggt ggagaggatg ggatgagaac aagaggctac ctccagttaa    1477

ccaggacata aagtccccag cggttcctgt cacacctgct cctccctccc cagggtgcat   1537

ccatgatcgt ggatgtttgc ccaggggtga ccatgtttgg ctggcttgga atgctgtgca   1597

ttctcagagc tctgttagtg tcccctcttg ggggtcagag atgaggtgtg cagggtcta    1657

gaggaatgag tgtccaggca gagttcagaa ggtaggaatg tccctcttga tagggctgaa   1717

tcaagggatt cctggcttta gaaagggtct gctatctttg caaaaatgtg caagtatctg   1777

tagccagtgt aatgaaatca cttccaaatc caaaaaaaaa aaaaaaaaaa aaaaaaaaaa   1837

aa                                                                 1839
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<210> 2
<211> 351
<212> PRT
<213> homo sapiens

<400> 2

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Met Thr Gly Ser His Asp Val Ile Gly Gly Ala Gly Lys Gln Val Leu
1               5                   10                  15


Cys Cys Phe Cys Lys Gln Arg Asn Lys Ser Leu Gly Thr Tyr Pro Gly
            20                  25                  30


Val Pro Gly Asn Ala Leu Trp Leu Leu Thr Ser Pro Ala Cys Asn Ala
        35                  40                  45


Leu Ser Thr Ser Ala Val Met His Gly Arg Asp Lys Gly Ser Val Thr
    50                  55                  60


His Gly Thr Val Gln Val Leu Ser Asp Thr Arg Phe Phe Ser Cys Arg
65                  70                  75                  80
```

3

```
Glu Gly Leu Leu Pro Ala Thr Gln Ser Pro Ala Met Ser Asp Pro Ile
                85                90                    95

Thr Leu Asn Val Gly Gly Lys Leu Tyr Thr Thr Ser Leu Ala Thr Leu
                100               105               110

Thr Ser Phe Pro Asp Ser Met Leu Gly Ala Met Phe Ser Gly Lys Met
            115               120               125

Pro Thr Lys Arg Asp Ser Gln Gly Asn Cys Phe Ile Asp Arg Asp Gly
    130               135               140

Lys Val Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser His Leu Asp
145               150               155               160

Leu Pro Glu Asp Phe Gln Glu Met Gly Leu Leu Arg Arg Glu Ala Asp
                165               170               175

Phe Tyr Gln Val Gln Pro Leu Ile Glu Ala Leu Gln Glu Lys Glu Val
            180               185               190

Glu Leu Ser Lys Ala Glu Lys Asn Ala Met Leu Asn Ile Thr Leu Asn
            195               200               205

Gln Arg Val Gln Thr Val His Phe Thr Val Arg Glu Ala Pro Gln Ile
    210               215               220

Tyr Ser Leu Ser Ser Ser Ser Met Glu Val Phe Asn Ala Asn Ile Phe
225               230               235               240

Ser Thr Ser Cys Leu Phe Leu Lys Leu Leu Gly Ser Lys Leu Phe Tyr
            245               250               255

Cys Ser Asn Gly Asn Leu Ser Ser Ile Thr Ser His Leu Gln Asp Pro
            260               265               270

Asn His Leu Thr Leu Asp Trp Val Ala Asn Val Glu Gly Leu Pro Glu
        275               280               285

Glu Glu Tyr Thr Lys Gln Asn Leu Lys Arg Leu Trp Val Val Pro Ala
    290               295               300
```

4

Asn Lys Gln Ile Asn Ser Phe Gln Val Phe Val Glu Glu Val Leu Lys
305   310   315   320

Ile Ala Leu Ser Asp Gly Phe Cys Ile Asp Ser Ser His Pro His Ala
            325   330   335

Leu Asp Phe Met Asn Asn Lys Ile Ile Arg Leu Ile Arg Tyr Arg
            340   345   350

<210> 3
<211> 237
<212> PRT
<213> homo sapiens

<400> 3

Met Asp Asn Gly Asp Trp Gly Tyr Met Met Thr Asp Pro Val Thr Leu
1   5   10   15

Asn Val Gly Gly His Leu Tyr Thr Thr Ser Leu Thr Thr Leu Thr Arg
            20   25   30

Tyr Pro Asp Ser Met Leu Gly Ala Met Phe Gly Gly Asp Phe Pro Thr
        35   40   45

Ala Arg Asp Pro Gln Gly Asn Tyr Phe Ile Asp Arg Asp Gly Pro Leu
    50   55   60

Phe Arg Tyr Val Leu Asn Phe Leu Arg Thr Ser Glu Leu Thr Leu Pro
65   70   75   80

Leu Asp Phe Lys Glu Phe Asp Leu Leu Arg Lys Glu Ala Asp Phe Tyr
            85   90   95

Gln Ile Glu Pro Leu Ile Gln Cys Leu Asn Asp Pro Lys Pro Leu Tyr
            100   105   110

Pro Met Asp Thr Phe Glu Glu Val Val Glu Leu Ser Ser Thr Arg Lys
        115   120   125

Leu Ser Lys Tyr Ser Asn Pro Val Ala Val Ile Ile Thr Gln Leu Thr
    130   135   140

Ile Thr Thr Lys Val His Ser Leu Leu Glu Gly Ile Ser Asn Tyr Phe
145   150   155   160

Thr Lys Trp Asn Lys His Met Met Asp Thr Arg Asp Cys Gln Val Ser
            165   170   175

Phe Thr Phe Gly Pro Cys Asp Tyr His Gln Glu Val Ser Leu Arg Val
            180   185   190

His Leu Met Glu Tyr Ile Thr Lys Gln Gly Phe Thr Ile Arg Asn Thr

5

```
            195                      200                      205
Arg Val His His Met Ser Glu Arg Ala Asn Glu Asn Thr Val Glu His
    210                 215                 220

Asn Trp Thr Phe Cys Arg Leu Ala Arg Lys Thr Asp Asp
225                 230                 235
```

<210> 4
<211> 256
<212> PRT
<213> homo sapiens

<220>
<221> UNSURE
<222> (15)..(15)
<223> wherein "X" is equal to any amino acid.

<400> 4

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Met Ser Arg Pro Leu Ile Thr Arg Ser Pro Ala Ser Pro Leu Xaa Asn
1               5                   10                  15

Gln Gly Ile Pro Thr Pro Ala Gln Leu Thr Lys Ser Asn Ala Pro Val
            20                  25                  30

His Ile Asp Val Gly Gly His Met Tyr Thr Ser Ser Leu Ala Thr Leu
            35                  40                  45

Thr Lys Tyr Pro Glu Ser Arg Ile Gly Arg Leu Phe Asp Gly Thr Glu
    50                  55                  60

Pro Ile Val Leu Asp Ser Leu Lys Gln His Tyr Phe Ile Asp Arg Asp
65                  70                  75                  80

Gly Gln Met Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser Lys Leu
            85                  90                  95

Leu Ile Pro Asp Asp Phe Lys Asp Tyr Thr Leu Leu Tyr Glu Glu Ala
            100                 105                 110

Lys Tyr Phe Gln Leu Gln Pro Met Leu Leu Glu Met Glu Arg Trp Lys
            115                 120                 125

Gln Asp Arg Glu Thr Gly Arg Phe Ser Arg Pro Cys Glu Cys Leu Val
    130                 135                 140

Val Arg Val Ala Pro Asp Leu Gly Glu Arg Ile Thr Leu Ser Gly Asp
145                 150                 155                 160

Lys Ser Leu Ile Glu Glu Val Phe Pro Glu Ile Gly Asp Val Met Cys
            165                 170                 175

Asn Ser Val Asn Ala Gly Trp Asn His Asp Ser Thr His Val Ile Arg
            180                 185                 190
```

6

Phe Pro Leu Asn Gly Tyr Cys His Leu Asn Ser Val Gln Val Leu Glu
        195   200   205

Arg Leu Gln Gln Arg Gly Phe Glu Ile Val Gly Ser Cys Gly Gly Gly
        210   215   220

Val Asp Ser Ser Gln Phe Ser Glu Tyr Val Leu Arg Arg Glu Leu Arg
225   230   235   240

Arg Thr Pro Arg Val Pro Ser Val Ile Arg Ile Lys Gln Glu Pro Leu
            245   250   255

<210> 5
<211> 234
<212> PRT
<213> homo sapiens

<400> 5

Met Pro His Arg Lys Glu Arg Pro Ser Gly Ser Ser Leu His Thr His
1   5   10   15

Gly Ser Thr Gly Thr Ala Glu Gly Gly Asn Met Ser Arg Leu Ser Leu
            20   25   30

Thr Arg Ser Pro Val Ser Pro Leu Ala Ala Gln Gly Ile Pro Leu Pro
        35   40   45

Ala Gln Leu Thr Lys Ser Asn Ala Pro Val His Ile Asp Val Gly Ser
        50   55   60

His Met Tyr Thr Ser Ser Leu Ala Thr Leu Thr Lys Tyr Pro Asp Ser
65   70   75   80

Arg Ile Ser Arg Leu Phe Asn Gly Thr Glu Pro Ile Val Leu Asp Ser
            85   90   95

Leu Lys Gln His Tyr Phe Ile Asp Arg Asp Gly Glu Ile Phe Arg Tyr
            100   105   110

Val Leu Ser Phe Leu Arg Thr Ser Lys Leu Leu Leu Pro Asp Asp Phe
        115   120   125

Lys Asp Phe Ser Leu Leu Tyr Glu Glu Ala Arg Tyr Tyr Gln Leu Gln
        130   135   140

Pro Met Val Arg Glu Leu Glu Arg Trp Gln Gln Glu Gln Glu Gln Arg
145   150   155   160

Arg Arg Ser Arg Ala Cys Asp Cys Leu Val Val Arg Val Thr Pro Asp
            165   170   175

Leu Gly Glu Arg Ile Ala Leu Ser Gly Glu Lys Ala Leu Ile Glu Glu
            180   185   190

Val Phe Pro Glu Thr Gly Asp Val Met Cys Asn Ser Val Asn Ala Gly
        195   200   205

Trp Asn Gln Asp Pro Thr His Val Ile Arg Phe Pro Leu Asn Gly Tyr
    210   215   220

Cys Arg Leu Asn Ser Val Gln Asp Val Leu
225   230

<210>   6
<211>   338
<212>   PRT
<213>   Drosophila melanogaster

<400>   6

Met Asp Arg Glu Arg Glu Arg Asp Val Lys Ala Leu Glu Pro Arg Asp
1   5   10   15

Leu Ser Ser Thr Gly Arg Ile Tyr Ala Arg Ser Asp Ile Lys Ile Ser
            20   25   30

Ser Ser Pro Thr Val Ser Pro Thr Ile Ser Asn Ser Ser Ser Pro Thr
            35   40   45

Pro Thr Pro Pro Ala Ser Ser Ser Val Thr Pro Leu Gly Leu Pro Gly
        50   55   60

Ala Val Ala Ala Ala Ala Ala Ala Val Gly Gly Ala Ser Ser Ala Gly
65   70   75   80

Ala Ser Ser Tyr Leu His Gly Asn His Lys Pro Ile Thr Gly Ile Pro
                85   90   95

Cys Val Ala Ala Ala Ser Arg Tyr Thr Ala Pro Val His Ile Asp Val
            100   105   110

Gly Gly Thr Ile Tyr Thr Ser Ser Leu Glu Thr Leu Thr Lys Tyr Pro
            115   120   125

Glu Ser Lys Leu Ala Lys Leu Phe Asn Gly Gln Ile Pro Ile Val Leu
    130   135   140

Asp Ser Leu Lys Gln His Tyr Phe Ile Asp Arg Asp Gly Gly Met Phe
145   150   155   160

Arg His Ile Leu Asn Phe Met Arg Asn Ser Arg Leu Leu Ile Ala Glu
                165   170   175

Asp Phe Pro Asp Leu Glu Leu Leu Leu Glu Glu Ala Arg Tyr Tyr Glu
                180   185   190

Val Glu Pro Met Ile Lys Gln Leu Glu Ser Met Arg Lys Asp Arg Val
            195   200   205

Arg Asn Gly Asn Tyr Leu Val Ala Pro Pro Thr Pro Pro Ala Arg His
    210   215   220

Ile Lys Thr Ser Pro Arg Thr Ser Ala Ser Pro Glu Cys Asn Tyr Glu

8

Val Val Ala Leu His Ile Ser Pro Asp Leu Gly Glu Arg Ile Met Leu
            245   250   255

Ser Ala Glu Arg Ala Leu Leu Asp Glu Leu Phe Pro Glu Ala Ser Gln
            260   265   270

Ala Thr Gln Ser Ser Arg Ser Gly Val Ser Trp Asn Gln Gly Asp Trp
            275   280   285

Gly Gln Ile Ile Arg Phe Pro Leu Asn Gly Tyr Cys Lys Leu Asn Ser
            290   295   300

Val Gln Val Leu Thr Arg Leu Leu Asn Ala Gly Phe Thr Ile Glu Ala
305   310   315   320

Ser Val Gly Gly Gln Gln Phe Ser Glu Tyr Leu Leu Ala Arg Arg Val
            325   330   335

Pro Met

<210>   7
<211>   733
<212>   DNA
<213>   homo sapiens

<400>   7
gggatccgga gcccaaatct tctgacaaaa ctcacacatg cccaccgtgc ccagcacctg   60

aattcgaggg tgcaccgtca gtcttcctct tccccccaaa acccaaggac accctcatga   120

tctcccggac tcctgaggtc acatgcgtgg tggtggacgt aagccacgaa gaccctgagg   180

tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg   240

aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact   300

ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca accccatcg   360

agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc   420

catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc aaaggcttct   480

atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga   540

ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag ctcaccgtgg   600

acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc   660

acaaccacta cacgcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc   720

gactctagag gat   733

<210>   8

<211> 724
<212> DNA
<213> homo sapiens

<220>
<221> Unsure
<222> (1)..(3)
<223> wherein "N" is equal to "A", "G", "C", or "T".

<400> 8
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nnnagtgaag ctaatgtact ttgcacagtg ttagcaatta tcacccattc atcaggtatt      60

aattcatttc gatcccaagg gcataggctt gatgtacaat aaggagttaa ggactgttaa     120

ttctctgata aggtttggtt atagtcattt ctcacttctc accctctcca ggactacttc     180

cagcaaccca gtctcctgcc atgtccgacc ccatcacgct gaacgtcggg gggaagctct     240

atacaacctc actggcgacc ctgaccagct tccctgactc catgctaggc gccatgttca     300

gcgggaagat gcccaccaag agggacagcc agggcaactg cttcattgac cgtgacggca     360

aagtgttccg ctatatcctc aacttcctgc ggacctccca ccttgacctg cctgaggact     420

tccaggagat ggggctgctc cgcagggagg ccgacttcta ccaggtgcag cccctgattg     480

aggccctgca ggagaaggaa gtggagctct ccaaggccga gaagaatgcc atgctcaaca     540

tcacactgaa ccagcgtgtg cagacggtcc acttcactgt gcgcgaggca ccccagatct     600

acagcctctc ctcttccagc atggaggtct tcaacgccaa catcttcagc acctcctgcc     660

tcttcctcaa gctccttggc tctaagctct ctactgctc caatggcaat ctctcctcca     720

tcac                                                                  724
```


<210> 9
<211> 74
<212> DNA
<213> homo sapiens

<400> 9
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ttgaggatat agcggaacac tttgccgtca cggtcaatga agcagttgcc ctggctgtcc      60

ctcttggtgg gcat                                                        74
```


<210> 10
<211> 20
<212> DNA
<213> homo sapiens

<400> 10
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atacaacctc actggcgacc                                                  20
```

10

```
<210>   11
<211>   20
<212>   DNA
<213>   homo sapiens

<400>   11
ccatctcctg gaagtcctca                                                    20


<210>   12
<211>   99
<212>   PRT
<213>   homo sapiens

<400>   12

Asp Pro Ile Thr Leu Asn Val Gly Gly Lys Leu Tyr Thr Thr Ser Leu
1                5                  10                  15

Ala Thr Leu Thr Ser Phe Pro Asp Ser Met Leu Gly Ala Met Phe Ser
            20                  25                  30

Gly Lys Met Pro Thr Lys Arg Asp Ser Gln Gly Asn Cys Phe Ile Asp
        35                  40                  45

Arg Asp Gly Lys Val Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser
        50                  55                  60

His Leu Asp Leu Pro Glu Asp Phe Gln Glu Met Gly Leu Leu Arg Arg
65                  70                  75                  80

Glu Ala Asp Phe Tyr Gln Val Gln Pro Leu Ile Glu Ala Leu Gln Glu
                85                  90                  95

Lys Glu Val


<210>   13
<211>   14
<212>   PRT
<213>   homo sapiens

<400>   13

Phe Cys Lys Gln Arg Asn Lys Ser Leu Gly Thr Tyr Pro Gly
1                5                  10

<210>   14
<211>   14
<212>   PRT
<213>   homo sapiens

<400>   14

Lys Asn Ala Met Leu Asn Ile Thr Leu Asn Gln Arg Val Gln
1                5                  10
```

11

<210> 15
<211> 14
<212> PRT
<213> homo sapiens

<400> 15

Tyr Cys Ser Asn Gly Asn Leu Ser Ser Ile Thr Ser His Leu
1   5   10

<210> 16
<211> 13
<212> PRT
<213> homo sapiens

<400> 16

Asp Thr Arg Phe Phe Ser Cys Arg Glu Gly Leu Leu Pro
1   5   10

<210> 17
<211> 13
<212> PRT
<213> homo sapiens

<400> 17

Leu Gly Ala Met Phe Ser Gly Lys Met Pro Thr Lys Arg
1   5   10

<210> 18
<211> 13
<212> PRT
<213> homo sapiens

<400> 18

Ser Gly Lys Met Pro Thr Lys Arg Asp Ser Gln Gly Asn
1   5   10

<210> 19
<211> 13
<212> PRT
<213> homo sapiens

<400> 19

Gln Thr Val His Phe Thr Val Arg Glu Ala Pro Gln Ile
1   5   10

<210> 20
<211> 26
<212> PRT
<213> homo sapiens

<400> 20

```
Gly Thr Tyr Pro Gly Val Pro Gly Asn Ala Leu Trp Leu Leu Thr Ser
1               5                   10                  15

Pro Ala Cys Asn Ala Leu Ser Thr Ser Ala
            20                  25
```

<210> 21
<211> 25
<212> PRT
<213> homo sapiens

<400> 21

```
Val Phe Asn Ala Asn Ile Phe Ser Thr Ser Cys Leu Phe Leu Lys Leu
1               5                   10                  15

Leu Gly Ser Lys Leu Phe Tyr Cys Ser
            20                  25
```

<210> 22
<211> 8
<212> PRT
<213> bacteriophage T7

<400> 22

```
Asp Tyr Lys Asp Asp Asp Asp Lys
1               5
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<210> 23
<211> 2154
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (1)..(1029)

<400> 23
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atg acg atg gcg gtt ttg cgg aat aga aaa ggg gga aag gga cca ctc        48
Met Thr Met Ala Val Leu Arg Asn Arg Lys Gly Gly Lys Gly Pro Leu
1               5                   10                  15

agg cgc cgg ccg ctg gcg ctg cct gct ctt cga ctg ggc gag ctt cct        96
Arg Arg Arg Pro Leu Ala Leu Pro Ala Leu Arg Leu Gly Glu Leu Pro
            20                  25                  30

gcc aat cag ggc gga acc agc gcg gcg tcg gcc agt agc ggg agg cgg       144
Ala Asn Gln Gly Gly Thr Ser Ala Ala Ser Ala Ser Ser Gly Arg Arg
            35                  40                  45

tcg ggt cag gcc cca gct ggg cgc gag cgg gtc ggc gtt gag gga gcc       192
Ser Gly Gln Ala Pro Ala Gly Arg Glu Arg Val Gly Val Glu Gly Ala
        50                  55                  60

acc gcc ctc ccg cct gcg cac tgc ctc tcg ccc ccc tcc ggc cag ccc       240
```

```
Thr Ala Leu Pro Pro Ala His Cys Leu Ser Pro Pro Ser Gly Gln Pro
65              70              75                      80

gca gcc ggc cgc gtc atg cca ggc gct gct cgg cga gcc aga ggg atg      288
Ala Ala Gly Arg Val Met Pro Gly Ala Ala Arg Arg Ala Arg Gly Met
                85                  90                  95

gtg gta gtc acg ggg cgg gag cca gac agc cgt cgt cag gac ggt gcc      336
Val Val Val Thr Gly Arg Glu Pro Asp Ser Arg Arg Gln Asp Gly Ala
                100                 105                 110

atg tcc agc tct gac gcc gaa gac gac ttt ctg gag ccg gcc acg ccg      384
Met Ser Ser Ser Asp Ala Glu Asp Asp Phe Leu Glu Pro Ala Thr Pro
            115                 120                 125

acg gcc acg cag gcg ggg cac gcg ctg ccc ctg ctg cca cag gag ttt      432
Thr Ala Thr Gln Ala Gly His Ala Leu Pro Leu Leu Pro Gln Glu Phe
        130                 135                 140

cct gag gtt gtt ccc ctt aac atc gga ggg gct cac ttc act aca cgc      480
Pro Glu Val Val Pro Leu Asn Ile Gly Gly Ala His Phe Thr Thr Arg
145                 150                 155                 160

ctg tcc aca ctg cgg tgc tac gaa gac acc atg ttg gca gcc atg ttc      528
Leu Ser Thr Leu Arg Cys Tyr Glu Asp Thr Met Leu Ala Ala Met Phe
                165                 170                 175

agt ggg cgg cac tac atc ccc aca gac tcc gag ggc cgg tac ttc atc      576
Ser Gly Arg His Tyr Ile Pro Thr Asp Ser Glu Gly Arg Tyr Phe Ile
                180                 185                 190

gac cga gat ggc aca cac ttt gga gat gtg ctg aat ttc ctg cgc tca      624
Asp Arg Asp Gly Thr His Phe Gly Asp Val Leu Asn Phe Leu Arg Ser
            195                 200                 205

ggg gac ctc cca ccc agg gag cgt gtt cga gct gtg tac aaa gag gcc      672
Gly Asp Leu Pro Pro Arg Glu Arg Val Arg Ala Val Tyr Lys Glu Ala
        210                 215                 220

cag tac tat gcc atc ggg ccc ctc ctg gag cag ctg gag aac atg cag      720
Gln Tyr Tyr Ala Ile Gly Pro Leu Leu Glu Gln Leu Glu Asn Met Gln
225                 230                 235                 240

cca ctg aag ggc gag aag gtg cgc caa gcg ttt ctg gga ctc atg ccc      768
Pro Leu Lys Gly Glu Lys Val Arg Gln Ala Phe Leu Gly Leu Met Pro
                245                 250                 255

tat tac aaa gac cac ttg gag cgg att gtg gag atc gcc cgg ctg cgt      816
Tyr Tyr Lys Asp His Leu Glu Arg Ile Val Glu Ile Ala Arg Leu Arg
            260                 265                 270

gcg gtc cag cgg aag gcc cgc ttt gcc aag ctc aag agc ttg aca cct      864
Ala Val Gln Arg Lys Ala Arg Phe Ala Lys Leu Lys Ser Leu Thr Pro
        275                 280                 285

tcc tgg cta atg agt gtc ctc atc aag atg ccc cct gga gtc aca tca      912
Ser Trp Leu Met Ser Val Leu Ile Lys Met Pro Pro Gly Val Thr Ser
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tgg att aac gca gaa agg cgg ctg tat ttg gaa act ccc att ggt cca     960
Trp Ile Asn Ala Glu Arg Arg Leu Tyr Leu Glu Thr Pro Ile Gly Pro
305                 310                 315                 320

gag aga cag aac aat gag aag aaa tcc cct gtc cag ttg cct gca gga    1008
Glu Arg Gln Asn Asn Glu Lys Lys Ser Pro Val Gln Leu Pro Ala Gly
                325                 330                 335

gta ttc caa cac ttc atg ggc tagaggattc cattgagatg gggtttacgt      1059
Val Phe Gln His Phe Met Gly
                340

cttgattttg aacacctgtc agcactgttc tctgtttgca tggcaattct gacccttta   1119

tggcaacaac acccctggga caacccagat ttgtagattg agatccaaag gtagaatttc   1179

cagacagtcc aaccaaggta tcaagtgatg tttccagagt ggaaggctct caccgtgtcc   1239

caggatttct ggggtttgta agcagtactg gccatttgtg accctgtttt ttacctaatc   1299

attctgtctt tttaggacat ggttttaccc gatccctggc aaaggatcca gaattccaat   1359

agctgaaaac cctgttatag cttttctcct attctgcctt acccaagaca cacttgaacc   1419

cctcagtaag gctatagaga gggccatgag caggggcagc ctctcccttg tttctacagc   1479

tccatgatga ggggttgact gaggccagca atccttgtag gtgtgacagt tgcaatataa   1539

ttaacagttt caagatctag aggtaccttt tgaaagaacc ccttcaggga tatctatcca   1599

cagtagcctg gagcagccaa ggtgaacctg agattttgac ccacacaata aggggggggcc   1659

attctttttc aaatattttg gcttcagaat acacttcatt acacatgcaa atattgagag   1719

attaacagaa attccagctc ttatgcctaa ctgagaagag ccactgcaag ttgcagttag   1779

gtaccatgt gcagcagagg ccagctgaat cccagagctt cccaaagtgg acaccagcgg   1839

ggactattcc tgatgtccca cccaagagag gaagatgagc tgaggcgctc ttgctctgcc   1899

caaatgcatc ccatgtgcat tcacgtgtca cccattcaaa ataacatggc attcttggaa   1959

ccttgtatct gacatgtaag accagcctac acattggggt gggtgcaggg gctcacactt   2019

gtaatcctag cactttggaa ggctgaggtg ggcagattgc ttgagcacag gagttccaga   2079

ccagcctgag caacatggcg aaatcctgtc tcttcaagaa ataaaataat aataataata   2139

aaaaaaaaaa aaaaa                                                    2154
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<212> PRT
<213> homo sapiens

15

<400> 24

Met Thr Met Ala Val Leu Arg Asn Arg Lys Gly Gly Lys Gly Pro Leu
1   5   10   15

Arg Arg Arg Pro Leu Ala Leu Pro Ala Leu Arg Leu Gly Glu Leu Pro
            20   25   30

Ala Asn Gln Gly Gly Thr Ser Ala Ala Ser Ala Ser Ser Gly Arg Arg
        35   40   45

Ser Gly Gln Ala Pro Ala Gly Arg Glu Arg Val Gly Val Glu Gly Ala
        50   55   60

Thr Ala Leu Pro Pro Ala His Cys Leu Ser Pro Pro Ser Gly Gln Pro
65   70   75   80

Ala Ala Gly Arg Val Met Pro Gly Ala Ala Arg Arg Ala Arg Gly Met
            85   90   95

Val Val Val Thr Gly Arg Glu Pro Asp Ser Arg Arg Gln Asp Gly Ala
            100   105   110

Met Ser Ser Ser Asp Ala Glu Asp Asp Phe Leu Glu Pro Ala Thr Pro
        115   120   125

Thr Ala Thr Gln Ala Gly His Ala Leu Pro Leu Leu Pro Gln Glu Phe
    130   135   140

Pro Glu Val Val Pro Leu Asn Ile Gly Gly Ala His Phe Thr Thr Arg
145   150   155   160

Leu Ser Thr Leu Arg Cys Tyr Glu Asp Thr Met Leu Ala Ala Met Phe
            165   170   175

Ser Gly Arg His Tyr Ile Pro Thr Asp Ser Glu Gly Arg Tyr Phe Ile
            180   185   190

Asp Arg Asp Gly Thr His Phe Gly Asp Val Leu Asn Phe Leu Arg Ser
        195   200   205

Gly Asp Leu Pro Pro Arg Glu Arg Val Arg Ala Val Tyr Lys Glu Ala
    210   215   220

16

Gln Tyr Tyr Ala Ile Gly Pro Leu Leu Glu Gln Leu Glu Asn Met Gln
225   230   235   240

Pro Leu Lys Gly Glu Lys Val Arg Gln Ala Phe Leu Gly Leu Met Pro
                 245   250   255

Tyr Tyr Lys Asp His Leu Glu Arg Ile Val Glu Ile Ala Arg Leu Arg
             260   265   270

Ala Val Gln Arg Lys Ala Arg Phe Ala Lys Leu Lys Ser Leu Thr Pro
         275   280   285

Ser Trp Leu Met Ser Val Leu Ile Lys Met Pro Pro Gly Val Thr Ser
    290   295   300

Trp Ile Asn Ala Glu Arg Arg Leu Tyr Leu Glu Thr Pro Ile Gly Pro
305   310   315   320

Glu Arg Gln Asn Asn Glu Lys Lys Ser Pro Val Gln Leu Pro Ala Gly
             325   330   335

Val Phe Gln His Phe Met Gly
         340

<210>   25
<211>   225
<212>   PRT
<213>   homo sapiens

<400>   25

Met Ser Thr Val Val Glu Leu Asn Val Gly Gly Glu Phe His Thr Thr
1   5   10   15

Thr Leu Gly Thr Leu Arg Lys Phe Pro Gly Ser Lys Leu Ala Glu Met
             20   25   30

Phe Ser Ser Leu Ala Lys Ala Ser Thr Asp Ala Glu Gly Arg Phe Phe
         35   40   45

Ile Asp Arg Pro Ser Thr Tyr Phe Arg Pro Ile Leu Asp Tyr Leu Arg
    50   55   60

Thr Gly Gln Val Pro Thr Gln His Ile Pro Glu Val Tyr Arg Glu Ala
65   70   75   80

Gln Phe Tyr Glu Ile Lys Pro Leu Val Lys Leu Leu Glu Asp Met Pro

17

```
                    85                      90                      95

Gln Ile Phe Gly Glu Gln Val Ser Arg Lys Gln Phe Leu Leu Gln Val
            100             105             110

Pro Gly Tyr Ser Glu Asn Leu Glu Leu Met Val Arg Leu Ala Arg Ala
            115             120             125

Glu Ala Ile Thr Ala Arg Lys Ser Ser Val Leu Val Cys Leu Val Glu
        130             135             140

Thr Glu Glu Gln Asp Ala Tyr Tyr Ser Glu Val Leu Cys Phe Leu Gln
145             150             155             160

Asp Lys Lys Met Phe Lys Ser Val Val Lys Phe Gly Pro Trp Lys Ala
                165             170             175

Val Leu Asp Asn Ser Asp Leu Met His Cys Leu Glu Met Asp Ile Lys
            180             185             190

Ala Gln Gly Tyr Lys Val Phe Ser Lys Phe Tyr Leu Thr Tyr Pro Thr
            195             200             205

Lys Arg Asn Glu Phe His Phe Asn Ile Tyr Ser Phe Thr Phe Thr Trp
    210             215             220

Trp
225

<210>   26
<211>   313
<212>   PRT
<213>   homo sapiens

<400>   26

Met Glu Glu Met Ser Gly Glu Ser Val Val Ser Ser Ala Val Pro Ala
1               5               10              15

Ala Ala Thr Arg Thr Thr Ser Phe Lys Gly Thr Ser Pro Ser Ser Lys
            20              25              30

Tyr Val Lys Leu Asn Val Gly Gly Ala Leu Tyr Tyr Thr Thr Met Gln
        35              40              45

Thr Leu Thr Lys Gln Asp Thr Met Leu Lys Ala Met Phe Ser Gly Arg
    50              55              60

Met Glu Val Leu Thr Asp Ser Glu Gly Trp Ile Leu Ile Asp Arg Cys
65              70              75              80

Gly Lys His Phe Gly Thr Ile Leu Asn Tyr Leu Arg Asp Gly Ala Val
            85              90              95

Pro Leu Pro Glu Ser Arg Arg Glu Ile Glu Glu Leu Leu Ala Glu Ala
            100             105             110
```

```
Lys Tyr Tyr Leu Val Gln Gly Leu Val Glu Glu Cys Gln Ala Ala Leu
        115                 120                 125

Gln Asn Lys Asp Thr Tyr Glu Pro Phe Cys Lys Val Pro Val Ile Thr
        130                 135                 140

Ser Ser Lys Glu Glu Gln Lys Leu Ile Ala Thr Ser Asn Lys Pro Ala
145                 150                 155                 160

Val Lys Leu Leu Tyr Asn Arg Ser Asn Asn Lys Tyr Ser Tyr Thr Ser
        165                 170                 175

Asn Ser Asp Asp Asn Met Leu Lys Asn Ile Glu Leu Phe Asp Lys Leu
        180                 185                 190

Ser Leu Arg Phe Asn Gly Arg Val Leu Phe Ile Lys Asp Val Ile Gly
        195                 200                 205

Asp Glu Ile Cys Cys Trp Ser Phe Tyr Gly Gln Gly Arg Lys Ile Ala
    210                 215                 220

Glu Val Cys Cys Thr Ser Ile Val Tyr Ala Thr Glu Lys Lys Gln Thr
225                 230                 235                 240

Lys Val Glu Phe Pro Glu Ala Arg Ile Tyr Glu Glu Thr Leu Asn Ile
            245                 250                 255

Leu Leu Tyr Glu Ala Gln Asp Gly Arg Gly Pro Asp Asn Ala Leu Leu
        260                 265                 270

Glu Ala Thr Gly Gly Ala Ala Gly Arg Ser His His Leu Asp Glu Asp
        275                 280                 285

Glu Glu Arg Glu Arg Ile Glu Arg Val Arg Arg Ile His Ile Lys Arg
    290                 295                 300

Pro Asp Asp Arg Ala His Leu His Gln
305                 310
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<210>   27
<211>   301
<212>   PRT
<213>   Drosophila melanogaster

<400>   27
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Met Ser Glu Ser Met Ser Gly Asp His Lys Ile Leu Leu Lys Gly His
1               5                   10                  15

Ser Ser Gln Tyr Leu Lys Leu Asn Val Gly Gly His Leu Tyr Tyr Thr
            20                  25                  30

Thr Ile Gly Thr Leu Thr Lys Asn Asn Asp Thr Met Leu Ser Ala Met
            35                  40                  45

Phe Ser Gly Arg Met Glu Val Leu Thr Asp Ser Glu Gly Trp Ile Leu
    50                  55                  60
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Ile Asp Arg Cys Gly Asn His Phe Gly Ile Ile Leu Asn Tyr Leu Arg
65                  70                  75                  80

Asp Gly Thr Val Pro Leu Pro Glu Thr Asn Lys Glu Ile Ala Glu Leu
                85                  90                  95

Leu Ala Glu Ala Lys Tyr Tyr Cys Ile Thr Glu Leu Ala Ile Ser Cys
            100                 105                 110

Glu Arg Ala Leu Tyr Ala His Gln Glu Pro Lys Pro Ile Cys Arg Ile
            115                 120                 125

Pro Leu Ile Thr Ser Gln Lys Glu Glu Gln Leu Leu Leu Ser Val Ser
    130                 135                 140

Leu Lys Pro Ala Val Ile Leu Val Val Gln Arg Gln Asn Asn Lys Tyr
145                 150                 155                 160

Ser Tyr Thr Ser Thr Ser Asp Asp Asn Leu Leu Lys Asn Ile Glu Leu
            165                 170                 175

Phe Asp Lys Leu Ser Leu Arg Phe Asn Glu Arg Ile Leu Phe Ile Lys
            180                 185                 190

Asp Val Ile Gly Pro Ser Glu Ile Cys Cys Trp Ser Phe Tyr Gly His
        195                 200                 205

Gly Lys Lys Val Ala Glu Val Cys Cys Thr Ser Ile Val Tyr Ala Thr
    210                 215                 220

Asp Arg Lys His Thr Lys Val Glu Phe Pro Glu Ala Arg Ile Tyr Glu
225                 230                 235                 240

Glu Thr Leu Gln Val Leu Leu Tyr Glu Asn Arg Asn Ala Pro Asp Gln
            245                 250                 255

Glu Leu Met Gln Ala Thr Ser Ser Ala Arg Val Gly Ser Ala Ser Gly
            260                 265                 270

Thr Ser Ile Asn Gln Tyr Thr Ser Asp Glu Glu Glu Glu Arg Thr Gly
        275                 280                 285

Leu Ala Arg Leu Arg Ser Asn Lys Arg Asn Asn Pro Ser
    290                 295                 300

<210>   28
<211>   221
<212>   PRT
<213>   Caenorhabditis elegans

<400>   28

Met Glu Pro Ser Thr Ile Val Lys Leu Asp Val Gly Gly Lys Ile Phe
1               5                   10                  15

Lys Thr Thr Ile Phe Thr Leu Cys Lys His Asp Ser Met Leu Lys Thr
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20

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                20                      25                      30
Met Phe Cys Thr Asp Val Pro Val Thr Lys Asn Glu Glu Gly Ser Val
        35                  40                  45

Phe Ile Asp Arg Asp Ser Lys His Phe Arg Leu Ile Leu Asn Phe Leu
    50                  55                  60

Arg Asp Gly Gln Ile Ala Leu Pro Asp Ser Asp Arg Glu Val Arg Glu
65                  70                  75                  80

Val Leu Ala Glu Ala Ser Tyr Phe Leu Leu Asp Pro Leu Ile Glu Leu
            85                  90                  95

Cys Gly Glu Arg Leu Glu Gln Ser Leu Asn Pro Tyr Tyr His Leu Val
            100                 105                 110

Ser Thr Val Leu Glu Ala Arg Lys Ile Ile Phe Ala Thr Glu Lys Pro
            115                 120                 125

Ile Val Val Leu Arg Leu Pro Val Tyr Ile Ala Thr Ser Gly Asn Gln
    130                 135                 140

Ser Tyr Tyr Phe Ser Glu Thr Lys Phe Arg Glu Leu Ser Glu Glu Tyr
145                 150                 155                 160

His Lys His Val Ala Phe Ile Leu Ile Thr Glu Pro Glu Phe Asn Glu
            165                 170                 175

Asp Cys Ser Trp Ser Phe Phe Leu Arg Ala Lys Lys Ile Thr Ala Arg
            180                 185                 190

Ile Lys Gly Pro Met Asp Cys Asn Leu Val Glu Glu Cys Met Pro Lys
            195                 200                 205

Thr Val Glu Arg Arg Arg Glu Lys Lys Thr Trp His His
    210                 215                 220
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agagaagaaa gtgttcagat ggacccgtgg gcttgagtga ctgaatgaat ggtgtggcac   120

caatcagacc ccagggattg aagatggagc agccccagct ctcattcccc gttgcctgcc   180

tgagagccct ggtgatttct ttccagtttc ctgaggttgt tccccttaac atcggagggg   240

ctcacttcac tacacgcctg tccacactgc ggtgctacga agacaccatg ttggcagcca   300

tgttcagtgg gcggcactac atccccacgg actccgaggg ccggtacttc atcgaccgag   360

atggcacaca ctttgggtat gtctctccct ctacaatcaa ctttgtagtc ctagcaggtg   420
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caacatggtg tcttcgtagc   80

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<213> homo sapiens

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tgttcccctt aacatcggag   20

<210> 32
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<400> 32
catacccaaa gtgtgtgcca   20

<210> 33
<211> 13
<212> PRT
<213> homo sapiens

<400> 33

Ala Ala Ser Ala Ser Ser Gly Arg Arg Ser Gly Gln Ala
1   5   10

<210> 34
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<400> 34

Gly Met Val Val Val Thr Gly Arg Glu Pro Asp Ser Arg
1   5   10

22

<210> 35
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<400> 35

Gly Arg Glu Pro Asp Ser Arg Arg Gln Asp Gly Ala Met
1   5   10

<210> 36
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<400> 36

Gly Gly Ala His Phe Thr Thr Arg Leu Ser Thr Leu Arg
1   5   10

<210> 37
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<213> homo sapiens

<400> 37

Thr Thr Arg Leu Ser Thr Leu Arg Cys Tyr Glu Asp Thr
1   5   10

<210> 38
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<400> 38

Leu Ala Ala Met Phe Ser Gly Arg His Tyr Ile Pro Thr
1   5   10

<210> 39
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<212> PRT
<213> homo sapiens

<400> 39

Glu Val Val Pro Leu Asn Ile Gly Gly Ala His Phe Thr Thr Arg Leu
1   5   10   15

Ser Thr Leu Arg Cys Tyr Glu Asp Thr Met Leu Ala Ala Met Phe Ser
             20   25   30

Gly Arg His Tyr Ile Pro Thr Asp Ser Glu Gly Arg Tyr Phe Ile Asp
             35   40   45

Arg Asp Gly Thr His Phe Gly Asp Val Leu Asn Phe Leu Arg Ser Gly

23

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    50                    55                    60
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Asp Leu Pro Pro Arg Glu Arg Val Arg Ala Val Tyr Lys Glu Ala Gln
65   70   75   80

Tyr Tyr Ala Ile Gly Pro Leu Leu Glu Gln Leu Glu Asn Met Gln Pro
                85   90   95

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<213>   homo sapiens

<400>   40

Ala Lys Leu Lys Ser Leu Thr Pro Ser Trp Leu Met Ser Val Leu Ile
1   5   10   15

Lys Met Pro Pro Gly Val Thr Ser Trp
            20   25

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gcagcagtcg acgcccatga agtgttggaa tactcctg   38

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gcagcagcgg ccgcatgacg atggcggttt tgcggaatag aaaaggggg   49

<210>   44
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<400>   44
gcagcagtcg acctggaccg cacgcagccg ggcgatctcc   40

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tggaggtagc ctcttgttct cat                                        23


<210>    47
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ccatcctctc caccagggcc ttct                                       24


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tgccccctgg agtcacat                                              18


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<400>    49
ggaccaatgg gagtttccaa                                            20


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cagccgcctt tctgcgttaa tccat                                      25


<210>    51
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25

<213> homo sapiens

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1   5   10

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<210> 53
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cctgaagcct gacattccat   20

<210> 54
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actgcagccg attcattaat g   21

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<400> 55
gaattaatac gactcactat agggagatat catacacata cgatttag   48

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gaattaatac gactcactat agggagacat gattacgcca agctcgaa   48

<210> 57
<211> 21
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<213> Drosophila melanogaster

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tgtaaaacga cggccagtga a                                             21


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caggtgcagc tggtgcagtc tgg                                           23


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caggtcaact taagggagtc tgg                                           23


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<400>  62
gaggtgcagc tgttgcagtc tgc                                           23


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<400>  63
caggtacagc tgcagcagtc agg                                           23
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tgaagagacg gtgaccattg tccc                                      24


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tgaggagacg gtgaccaggg ttcc                                      24


<210>   67
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<400>   67
tgaggagacg gtgaccgtgg tccc                                      24


<210>   68
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gatattgtga tgactcagtc tcc   23

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gaaattgtgc tgactcagtc tcc   23

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<400>  78
tcttctgagc tgactcagga ccc                                             23


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cacgttatac tgactcaacc gcc                                             23


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caggctgtgc tcactcagcc gtc                                             23


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aattttatgc tgactcagcc cca                                             23


<210>  82
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acgtttgatt tccaccttgg tccc                                            24
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<210> 83
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<400> 83
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<210> 84
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<400> 84
acgtttgata tccactttgg tccc   24

<210> 85
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<400> 85
acgtttgatc tccaccttgg tccc   24

<210> 86
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<400> 86
acgtttaatc tccagtcgtg tccc   24

<210> 87
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<400> 87
cagtctgtgt tgacgcagcc gcc   23

<210> 88
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<400> 88
cagtctgccc tgactcagcc tgc   23

<210> 89
<211> 23

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<400>   89
tcctatgtgc tgactcagcc acc                                          23


<210>   90
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Ile Leu Val Thr Thr Val Leu Pro Leu Tyr Gln Lys Ser Val Trp Thr
            35   40   45

Gln Glu Ser Lys Cys His Leu Ile Glu Thr Asn Ile Arg Asp Gln Glu
    50   55   60

Glu Leu Lys Gly Lys Lys Val Pro Gln Tyr Pro Cys Leu Trp Val Asn
65   70   75   80

Val Ser Ala Ala Gly Arg Trp Ala Val Leu Tyr His Thr Glu Asp Thr
            85   90   95

Arg Asp Gln Asn Gln Gln Cys Ser Tyr Ile Pro Gly Ser Val Asp Asn
            100   105   110

Tyr Gln Thr Ala Arg Ala Asp Val Glu Lys Val Arg Ala Lys Phe Gln
        115   120   125

Glu Gln Gln Val Phe Tyr Cys Phe Ser Ala Pro Arg Gly Asn Glu Thr
    130   135   140

Ser Val Leu Phe Gln Arg Leu Tyr Gly Pro Gln Ala Leu Leu Phe Ser

33

145   150   155   160

Leu Phe Trp Pro Thr Phe Leu Leu Thr Gly Gly Leu Leu Ile Ile Ala
            165   170   175

Met Val Lys Ser Asn Gln Tyr Leu Ser Ile Leu Ala Ala Gln Lys
        180   185   190